OIPE

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/444,762

DATE: 12/13/1999
TIME: 23:45:23

INPUT SET: S34198.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

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1                                SEQUENCE LISTING
2
3   (1)    General Information
4
5          (i) APPLICANT: Bryan, Bruce
6
7          (ii) TITLE OF INVENTION: BIOLUMINESCENT ARTICLES OF  MANUFACTURE
8
9          (iii) NUMBER OF SEQUENCES: 14
10
11         (iv) CORRESPONDENCE ADDRESS:
12            (A) ADDRESSEE: Heller Ehrman White & McAuliffe
13            (B) STREET: 4250 Executive Square, 7th Floor
14            (C) CITY: La Jolla
15            (D) STATE: CA
16            (E) COUNTRY: USA
17            (F) ZIP: 92037
18
19         (v) COMPUTER READABLE FORM:
20            (A) MEDIUM TYPE: Diskette
21            (B) COMPUTER: IBM Compatible
22            (C) OPERATING SYSTEM: DOS
23            (D) SOFTWARE: FastSEQ Version 1.5
24
25         (vi) CURRENT APPLICATION DATA:
26            (A) APPLICATION NUMBER:
27            (B) FILING DATE:
28            (C) CLASSIFICATION:
29
30         (vii) PRIOR APPLICATION DATA:
31            (A) APPLICATION NUMBER: 0909/135,988
32            (B) FILING DATE: 08-17-98
33            (C) CLASSIFICATION:
34
35         (vii) PRIOR APPLICATION DATA:
36            (A) APPLICATION NUMBER: 08/757,046
37            (B) FILING DATE: 11-25-96
38            (C) CLASSIFICATION:
39
40         (vii) PRIOR APPLICATION DATA:
41            (A) APPLICATION NUMBER: 08/597,274
42            (B) FILING DATE: 02-06-96
43
44         (viii) ATTORNEY/AGENT INFORMATION:
45            (A) NAME: Seidman, Stephanie L
46            (B) REGISTRATION NUMBER: 33,779
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INPUT SET: S34198.raw

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47          (C)  REFERENCE/DOCKET NUMBER: 24727-105C
48
49       (ix) TELECOMMUNICATION INFORMATION:
50          (A)  TELEPHONE: 619-450-8400
51          (B)  TELEFAX: 619-450-8499
52          (C)  TELEX:
53
54         (2)  INFORMATION FOR SEQ ID NO:1:
55
56       (i)  SEQUENCE CHARACTERISTICS:
57          (A)  LENGTH: 1196 base pairs
58          (B)  TYPE: nucleic acid
59          (C)  STRANDEDNESS: single
60          (D)  TOPOLOGY: linear
61
62       (ii) MOLECULE TYPE: cDNA
63
64       (vi) ORIGINAL SOURCE:
65
66       (ix) FEATURE:
67
68          (A)  NAME/KEY: Coding Sequence
69          (B)  LOCATION: 1...942
70          (D)  OTHER INFORMATION: Renilla Reinformis Luciferase
71
72       (x)  PUBLICATION INFORMATION:
73
74          PATENT NO.: 5,418,155
75
76       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
77
78    AGC TTA AAG ATG ACT TCG AAA GTT TAT GAT CCA GAA CAA AGG AAA CGG        48
79    Ser Leu Lys Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg
80     1               5                   10                  15
81
82    ATG ATA ACT GGT CCG CAG TGG TGG GCC AGA TGT AAA CAA ATG AAT GTT        96
83    Met Ile Thr Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val
84                20                  25                  30
85
86    CTT GAT TCA TTT ATT AAT TAT TAT GAT TCA GAA AAA CAT GCA GAA AAT       144
87    Leu Asp Ser Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn
88                35                  40                  45
89
90    GCT GTT ATT TTT TTA CAT GGT AAC GCG GCC TCT TCT TAT TTA TGG CGA       192
91    Ala Val Ile Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg
92        50                  55                  60
93
94    CAT GTT GTG CCA CAT ATT GAG CCA GTA GCG CGG TGT ATT ATA CCA GAT       240
95    His Val Val Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp
96    65                  70                  75                  80
97
98    CTT ATT GGT ATG GGC AAA TCA GGC AAA TCT GGT AAT GGT TCT TAT AGG       288
99    Leu Ile Gly Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg
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INPUT SET: S34198.raw

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102    TTA CTT GAT CAT TAC AAA TAT CTT ACT GCA TGG TTG AAC TTC TTA ATT     336
103    Leu Leu Asp His Tyr Lys Tyr Leu Thr Ala Trp Leu Asn Phe Leu Ile
104                    100                     105                     110
105
106    TAC CAA AGA AGA TCA TTT TTT GTC GGC CAT GAT TGG GGT GCT TGT TTG     384
107    Tyr Gln Arg Arg Ser Phe Phe Val Gly His Asp Trp Gly Ala Cys Leu
108                    115                     120                     125
109
110    GCA TTT CAT TAT AGC TAT GAG CAT CAA GAT AAG ATC AAA GCA ATA GTT     432
111    Ala Phe His Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val
112                    130                     135                     140
113
114    CAC GCT GAA AGT GTA GTA GAT GTG ATT GAA TCA TGG GAT GAA TGG CCT     480
115    His Ala Glu Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro
116    145                     150                     155                     160
117
118    GAT ATT GAA GAA GAT ATT GCG TTG ATC AAA TCT GAA GAA GGA GAA AAA     528
119    Asp Ile Glu Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys
120                    165                     170                     175
121
122    ATG GTT TTG GAG AAT AAC TTC TTC GTG GAA ACC ATG TTG CCA TCA AAA     576
123    Met Val Leu Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys
124                    180                     185                     190
125
126    ATC ATG AGA AAG TTA GAA CCA GAA GAA TTT GCA GCA TAT CTT GAA CCA     624
127    Ile Met Arg Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro
128                    195                     200                     205
129
130    TTC AAA GAG AAA GGT GAA GTT CGT CGT CCA ACA TTA TCA TGG CCT CGT     672
131    Phe Lys Glu Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg
132                    210                     215                     220
133
134    GAA ATC CCG TTA GTA AAA GGT GGT AAA CCT GAC GTT GTA CAA ATT GTT     720
135    Glu Ile Pro Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val
136    225                     230                     235                     240
137
138    AGG AAT TAT AAT GCT TAT CTA CGT GCA AGT GAT GAT TTA CCA AAA ATG     768
139    Arg Asn Tyr Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met
140                    245                     250                     255
141
142    TTT ATT GAA TCG GAT CCA GGA TTC TTT TCC AAT GCT ATT GTT GAA GGC     816
143    Phe Ile Glu Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly
144                    260                     265                     270
145
146    GCC AAG AAG TTT CCT AAT ACT GAA TTT GTC AAA GTA AAA GGT CTT CAT     864
147    Ala Lys Lys Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His
148                    275                     280                     285
149
150    TTT TCG CAA GAA GAT GCA CCT GAT GAA ATG GGA AAA TAT ATC AAA TCG     912
151    Phe Ser Gln Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser
152                    290                     295                     300
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INPUT SET: S34198.raw

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153
154    TTC GTT GAG CGA GTT CTC AAA AAT GAA CAA TAA TTACTTTGGT TTTTTATTTA    965
155    Phe Val Glu Arg Val Leu Lys Asn Glu Gln
156    305                         310
157
158    CATTTTTCCC GGGTTTAATA ATATAAATGT CATTTTCAAC AATTTTATTT TAACTGAATA    1025
159    TTTCACAGGG AACATTCATA TATGTTGATT AATTTAGCTC GAACTTTACT CTGTCATATC    1085
160    ATTTTGGAAT ATTACCTCTT TCAATGAAAC TTTATAAACA GTGGTTCAAT TAATTAATAT    1145
161    ATATTATAAT TACATTTGTT ATGTAATAAA CTCGGTTTTA TTATAAAAAA A            1196
162
163              (2)  INFORMATION FOR SEQ ID NO:2:
164
165         (i)  SEQUENCE CHARACTERISTICS:
166              (A)  LENGTH: 1822 base pairs
167              (B)  TYPE: nucleic acid
168              (C)  STRANDEDNESS: single
169              (D)  TOPOLOGY: linear
170
171         (ii) MOLECULE TYPE: cDNA
172
173         (ix) FEATURE:
174
175              (A)  NAME/KEY: Coding Sequence
176              (B)  LOCATION: 1...1665
177              (D)  OTHER INFORMATION:  Cypridina hilgendorfii luciferase
178
179         (x)  PUBLICATION INFORMATION:
180
181              PATENT NO.:   EP 0 387 355 TORAY
182
183         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
184
185    ATG AAG CTA ATA ATT CTG TCT ATT ATA TTG GCC TAC TGT GTC ACA GTC    48
186    Met Lys Leu Ile Ile Leu Ser Ile Ile Leu Ala Tyr Cys Val Thr Val
187    1               5                   10                  15
188
189    AAC TGC CAG GAT GCA TGT CCT GTA GAA GCT GAA GCA CCG TCA AGT ACA    96
190    Asn Cys Gln Asp Ala Cys Pro Val Glu Ala Glu Ala Pro Ser Ser Thr
191            20                  25                  30
192
193    CCA ACA GTC CCA ACA TCT TGT GAA GCT AAA GAA GGA GAA TGT ATC GAT    144
194    Pro Thr Val Pro Thr Ser Cys Glu Ala Lys Glu Gly Glu Cys Ile Asp
195            35                  40                  45
196
197    ACC AGA TGC GCA ACA TGT AAA CGA GAC ATA CTA TCA GAC GGA CTG TGT    192
198    Thr Arg Cys Ala Thr Cys Lys Arg Asp Ile Leu Ser Asp Gly Leu Cys
199        50                  55                  60
200
201    GAA AAT AAA CCA GGG AAG ACA TGC TGT AGA ATG TGC CAG TAT GTA ATT    240
202    Glu Asn Lys Pro Gly Lys Thr Cys Cys Arg Met Cys Gln Tyr Val Ile
203    65                  70                  75                  80
204
205    GAA TCC AGA GTA GAA GCT GCT GGA TAT TTT AGA ACG TTT TAC GCC AAA    288
```

INPUT SET: S34198.raw

```
206   Glu Ser Arg Val Glu Ala Ala Gly Tyr Phe Arg Thr Phe Tyr Ala Lys
207                 85                  90                  95
208

209   AGA TTT AAT TTT CAG GAA CCT GGT AAA TAT GTG CTG GCT CGA GGA ACC      336
210   Arg Phe Asn Phe Gln Glu Pro Gly Lys Tyr Val Leu Ala Arg Gly Thr
211               100                 105                 110
212

213   AAG GGT GGC GAC TGG TCT GTA ACC CTC ACC ATG GAG AAT CTA GAT GGA      384
214   Lys Gly Gly Asp Trp Ser Val Thr Leu Thr Met Glu Asn Leu Asp Gly
215               115                 120                 125
216

217   CAG AAG GGA GCT GTA CTG ACT AAG ACA ACA CTG GAG GTA GTA GGA GAC      432
218   Gln Lys Gly Ala Val Leu Thr Lys Thr Thr Leu Glu Val Val Gly Asp
219         130                 135                 140
220

221   GTA ATA GAC ATT ACT CAA GCT ACT GCA GAT CCT ATC ACA GTT AAC GGA      480
222   Val Ile Asp Ile Thr Gln Ala Thr Ala Asp Pro Ile Thr Val Asn Gly
223   145                 150                 155                 160
224

225   GGA GCT GAC CCA GTT ATC GCT AAC CCG TTC ACA ATT GGT GAG GTG ACC      528
226   Gly Ala Asp Pro Val Ile Ala Asn Pro Phe Thr Ile Gly Glu Val Thr
227               165                 170                 175
228

229   ATT GCT GTT GTC GAA ATA CCC GGC TTC AAT ATT ACA GTC ATC GAA TTC      576
230   Ile Ala Val Val Glu Ile Pro Gly Phe Asn Ile Thr Val Ile Glu Phe
231               180                 185                 190
232

233   TTT AAA CTA ATC GTG ATA GAT ATT CTG GGA GGA AGA TCT GTG AGA ATT      624
234   Phe Lys Leu Ile Val Ile Asp Ile Leu Gly Gly Arg Ser Val Arg Ile
235               195                 200                 205
236

237   GCT CCA GAC ACA GCA AAC AAA GGA CTG ATA TCT GGT ATC TGT GGT AAT      672
238   Ala Pro Asp Thr Ala Asn Lys Gly Leu Ile Ser Gly Ile Cys Gly Asn
239         210                 215                 220
240

241   CTG GAG ATG AAT GAC GCT GAT GAC TTT ACT ACA GAC GCA GAT CAG CTG      720
242   Leu Glu Met Asn Asp Ala Asp Asp Phe Thr Thr Asp Ala Asp Gln Leu
243   225                 230                 235                 240
244

245   GCG ATC CAA CCC AAC ATA AAC AAA GAG TTC GAC GGC TGC CCA TTC TAC      768
246   Ala Ile Gln Pro Asn Ile Asn Lys Glu Phe Asp Gly Cys Pro Phe Tyr
247               245                 250                 255
248

249   GGG AAT CCT TCT GAT ATC GAA TAC TGC AAA GGT CTC ATG GAG CCA TAC      816
250   Gly Asn Pro Ser Asp Ile Glu Tyr Cys Lys Gly Leu Met Glu Pro Tyr
251               260                 265                 270
252

253   AGA GCT GTA TGT CGT AAC AAT ATC AAC TTC TAC TAT TAC ACT CTG TCC      864
254   Arg Ala Val Cys Arg Asn Asn Ile Asn Phe Tyr Tyr Tyr Thr Leu Ser
255         275                 280                 285
256

257   TGC GCC TTC GCT TAC TGT ATG GGA GGA GAA GAA AGA GCT AAA CAC GTC      912
258   Cys Ala Phe Ala Tyr Cys Met Gly Gly Glu Glu Arg Ala Lys His Val
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/09/444,762*

INPUT SET: S34198.raw

Line	Error	Original Text